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Analysis of archaeal communities in Gulf of Mexico dead zone sediments.

Sediments may contribute significantly to Louisiana continental shelf "dead zone" hypoxia but limited information hinders comparison of sediment biogeochemistry between norm-oxic and hypoxic seasons. Dead zone sediment cores collected during hypoxia (September 2006) had higher levels of NH₄⁺, Fe₂⁺ and dissolved inorganic carbon in porewater, and reduced solid iron, than cores collected in norm-oxic conditions (April 2006). These results suggest reduced end products of microbial respiration accumulated as oxygen diminished in the overlying water. In sediments, different microorganisms compete for the same electron donors and acceptors and against abiotic reactions. Analyses of microbial communities might help to differentiate processes taking place in the sediments. Archaea have been shown to dominate ammonium-oxidizer communities in marine systems. Therefore, pyrosequencing of 16S rRNA genes using Archaea-specific primers was undertaken to investigate archaeal community composition in the April and September 2006 sediment cores. Crenarchaeote sequences accounted for over half of the 260,000 sequences obtained. The most abundant cluster of genus-level (97% similarity) sequences contained that of an uncultured, Desulfurococcaceae-related archaeon. Sequences within the cluster accounted for 11% of all those obtained. They were most abundant in the deepest sediment core fractions (6 to 10 cm) collected during hypoxic conditions in September. The next three most abundant clusters included the ammonium-oxidizing archeaon, Nitrosopumilus and accounted for 15% of the total sequences. Nitrosopumilus clusters were most abundant in the upper 6 cm of sediment and were significantly higher in cores collected under normoxic conditions. These results reveal changes in the community structure of Archaea in the upper sediments, including abundance of Nitrosopumilus spp., which may be associated with the availability of oxygen needed for ammonium oxidation.